

FIGURE 1. FUP MSP-1 p42 amino acid sequence SEQ ID NO: 19

AISVTMDNIL SGFENEYDVI YLKPLAGVYR SLKKQIEKNI FTFNLNLNDI LNSRLKKRKY 60
FLDVLES DLM QFKHISSNEY IIEDSFKLLN SEQNTLLKS YKYIKESVEN DIKFAQEGIS 120
YYEKVLAKYK DDLESIKKVI KEEKEKFPSS PPTTPPSPAK TDEQKKESKF LPFLTNIETL 180
YNNLVNKIDD YLINLKAKIN DCNVEKDEAH VKITKLSDLK AIDDKIDLFK NHNDFEAIKK 240
LINDDTKKDM LGKLLSTGLV QNFPNTIISK LIEGKFQDML **NISQHQC**VKK **QCPENSGC**FR 300
HLDEREECKC **LLNYKQEGDK** **CVENPNPTCN** **ENNGGCDADA** **KCTEEDSGSN** **GKKITCECTK** 360
PDSYPLFDGI **FCS** 373

FIGURE 2. Alignment of the MSP-1 p42 amino acid sequences from the three *P. falciparum* strains FUP SEQ ID NO:19, 3D7 SEQ ID NO:20, and FVO SEQ ID NO:21.

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      10      20      30      40      50
      +-----+-----+-----+-----+
1 AIS-VTMDNILSGFENEYDVIYLKPLAGVYRSLKKQIEKNIFTFNLNLNDILNSRLKKRK FUP_P42
1 +++-+++++ 3D7_P42
1 +VTPSVI+++++KI++++E+L+++++L+++VM+++V+VK+++++N++E FVO_P42

      60      70      80      90     100     110
      +-----+-----+-----+-----+
60 YFLDVLES DLMQFKHISSNEYIIEDSFKLLNSEQKNTLLKSYKYIKESVENDIKFAQEGI FUP_P42
60 ++++++ 3D7_P42
61 N+KN+++++IPYKDLT+SN+VVK+PY+F++K+KRDKF+S++N+++DSIDT++N++NDVL FVO_P42

     120     130     140     150     160     170
     +-----+-----+-----+-----+
120 SYYEKVLAKYKDDLESIKKVIKEEKEKFPSSPPTTPPSPAKTDEQKESKFLPFLTNIET FUP_P42
120 ++++++ 3D7_P42
121 G++KILSE+++S++D+++Y+N-----+K+GENE+Y++++N++++ FVO_P42

     180     190     200     210     220     230
     +-----+-----+-----+-----+
180 LYNNLVNKIDDYLINLKAKINDCNVEKDEAHVKITKLSDLKAIDDKIDLFKNHNDFDAIK FUP_P42
180 ++++++ 3D7_P42
161 ++KTVND+++LFV+H+E++VLNYTY++SNVE+++KELNY++TIQ++LAD++KN+N+VG+A FVO_P42

     240     250     260     270     280     290
     +-----+-----+-----+-----+
240 KLINDDTKKDMLGKLLSTGLV-QNFPNTIISKLIEGKFQDMLNISQHQCVKKQCPENSGC FUP_P42
240 ++++++ 3D7_P42
221 D+ST+YNHNNL+TKF+++M+FENLAKTVL+N+LD+NL+G+++++Q++++ FVO_P42

     300     310     320     330     340     350
     +-----+-----+-----+-----+
299 FRHLDEREECKLLNYKQEGDKCVENPNPTCNENNGGCDADAKCTEEDSGSNGKITCEC FUP_P42
299 ++++++T+++++SR+++++ 3D7_P42
281 ++++++ FVO_P42

     360     370
     +-----+
359 TKPDSYPLFDGIFCS FUP_P42
359 ++++++ 3D7_P42
341 ++++++ FVO_P42

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	10	20	30	40	50	60	
	-----+-----+-----+-----+-----+						
1	AISVTMDNILSGFENEYDVIIY <u>LKPLAGVYRSLLKKQ</u> IEKNIFTFNLNLDIILNSRLKKRKY FUP_p42						
	70	80	90	100	110	120	
	-----+-----+-----+-----+-----+						
61	FLDVLESDLMQFKHISSNEYIIEDSFKLLNSEQKNTLLKSYYIKESVENDIKFAQEGIS FUP_p42						
	130	140	150	160	170	180	
	-----+-----+-----+-----+-----+						
121	YYEKVLAKYKDDLESIKKVIKEEKEKFPSSPPTTPPSPAKTDEQKESKFLPFLTNIETL FUP_p42						
	190	200	210	220	230	240	
	-----+-----+-----+-----+-----+						
181	YNNLVNKIDDYLENLKAKINDCNVEKDE <u>AHVKITKLSDLKAID</u> DKIDLFGKNHNDFDAIKK FUP_p42						
1	garsggggtAHVKITKLSDLKAIDDKIDLFGKNHNDFDAIKK Construct A						
1	gars <u>LKPLAGVYRSLLKKQ</u> ggggtAHVKITKLSDLKAIDDKIDLFGKNHNDFDAIKK Construct B						
	250	260	270	280	290	300	
	-----+-----+-----+-----+-----+						
241	LINDDTKKDMLGKLLSTGLVONFPNTTIISKLI E GKFQDMLNISQHQC V KKQCPENSGC F R FUP_p42						
42	LINDDTKKDMLGKLLSTGLVONFPNTTIISKLI E GKFQDMLNISQHQC V KKQCPENSGC F R Construct A						
59	LINDDTKKDMLGKLLSTGLVONFPNTTIISKLI E GKFQDMLNISQHQC V KKQCPENSGC F R Construct B						
1	garsggggtMKGKLLSTGLVONFPNTTIISKLI E GKFQDMLNISQHQC V KKQCPENSGC F R Construct C						
	310	320	330	340	350	360	
	-----+-----+-----+-----+-----+						
301	HLDEREECCKLLNYKQEGDKCVENPNPTCNENNNGGCCADAKCTEEDSGSNGKKITCECTK FUP_p42						
102	HLDEREECCKLLNYKQEGDKCVENPNPTCNENNNGGCCADATCTEEDSGSSRRKKITCECTK Construct A						
119	HLDEREECCKLLNYKQEGDKCVENPNPTCNENNNGGCCADATCTEEDSGSSRRKKITCECTK Construct B						
61	HLDEREECCKLLNYKQEGDKCVENPNPTCNENNNGGCCADAKCTEEDSGSNGKKITCECTK Construct C						
	370						
	-----+-----						
361	PDSYPLFDGIFCS FUP_p42						
162	PDSYPLFDGIFCS Construct A						
179	PDSYPLFDGIFCS Construct B						
121	PDSYPLFDGIFCS Construct C						

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10      20      30      40      50      60
-----+-----+-----+-----+-----+
1 AISVTMDNILSGFENEYDVIYLKPLAGVYRSLKKQIEKNIFTFNLNLNDILNSRLKKRKY FUP_p42
-----+-----+-----+-----+-----+
                               -LKPLAGVYRSLKKQ-
-----+-----+-----+-----+-----+
                               -LKPLAGVYRSLKKQ-
-----+-----+-----+-----+-----+
                               -LKPLAGVYRSLKKQ-
-----+-----+-----+-----+-----+
                               -LKPLAGVYRSLKKQ-
-----+-----+-----+-----+-----+
                               -LKPLAGVYRSLKKQ-
-----+-----+-----+-----+-----+
AISVTMDNILSGFENEYDVIYLKPLAGVYRSLKKQIEKNIFTFNLNLNDILNSRLKKRKY SEQ ID NO: 8 (H)
AISVTMDNILSGFENEYDVI----- SEQ ID NO: 9 (I)
AISVTMDNILSGFENEYDVIYLKPLAGVYRSLKKQIEKNI----- SEQ ID NO: 10 (J)
-----+-----+-----+-----+-----+
                               -LKPLAGVYRSLKKQ-
-----+-----+-----+-----+-----+
-----DNILS-----YLKPLAGVYRSLKKQI-----LNSRL----- SEQ ID NO: 14 (N)
AISVTM-----GFENEYDVI-----EKNIFTFNLNLNDI-----KKRKY SEQ ID NO: 15 (O)
-----+-----+-----+-----+-----+
                               -LKPLAGVYRSLKKQ-
-----+-----+-----+-----+-----+
AISVTMDNILSGFENEYDVI----- SEQ ID NO: 18 (R)

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	250	260	270	
	-----+-----+-----+-----			
241	LINDDTKKDMLGKLLSTGLVQNF	<u>PNTIISKLIEGKFQDML</u>		FUP_p42
	LINDDTKKDMLGKLLSTGLVQNF	PNTIISKLIEGKFQDML		SEQ ID NO:1 (A)
	LINDDTKKDMLGKLLSTGLVQNF	PNTIISKLIEGKFQDML		SEQ ID NO:2 (B)
	-----MLGKLLSTGLVQNF	PNTIISKLIEGKFQDML		SEQ ID NO:3 (C)
	LINDDTKKDMLGKLLSTGLVQNF	PNTIISKLIEGKFQDML		SEQ ID NO:4 (D)
	LINDDTKKDMLGKLLSTGLVQNF	PNTIISKLIEGKFQDML		SEQ ID NO:5 (E)
	LINDDTKKDMLGKLLSTGLVQNF	PNTIISKLIEGKFQDML		SEQ ID NO:6 (F)
	LINDDTKKDMLGKLLSTGLVQNF	PNTIISKLIEGKFQDML		SEQ ID NO:7 (G)
	LINDDTKKDMLG-----			SEQ ID NO:8 (H)
	LINDDTKKDMLG-----			SEQ ID NO:9 (I)
	LINDDTKKDMLG-----			SEQ ID NO:10 (J)
	LINDDTKKDMLG-----			SEQ ID NO:11 (K)
	LINDDTKKDMLG-----			SEQ ID NO:12 (L)
	-----			SEQ ID NO:13 (M)
	LINDDTKKDMLG-----			SEQ ID NO:14 (N)
	LINDDTKKDMLGKLLSTGLVQNF	PNTIISKLIEGKFQDML		SEQ ID NO:15 (O)
	LINDDTKKDMLG-----			SEQ ID NO:16 (P)
	LINDDTKKDMLGKLLSTGLVQNF	PNTIISKLIEGKFQDML		SEQ ID NO:17 (Q)
	-----			SEQ ID NO:18 (R)

Figure 5. Diagram of all MSP-1 C-terminal constructs -- ordered by Name

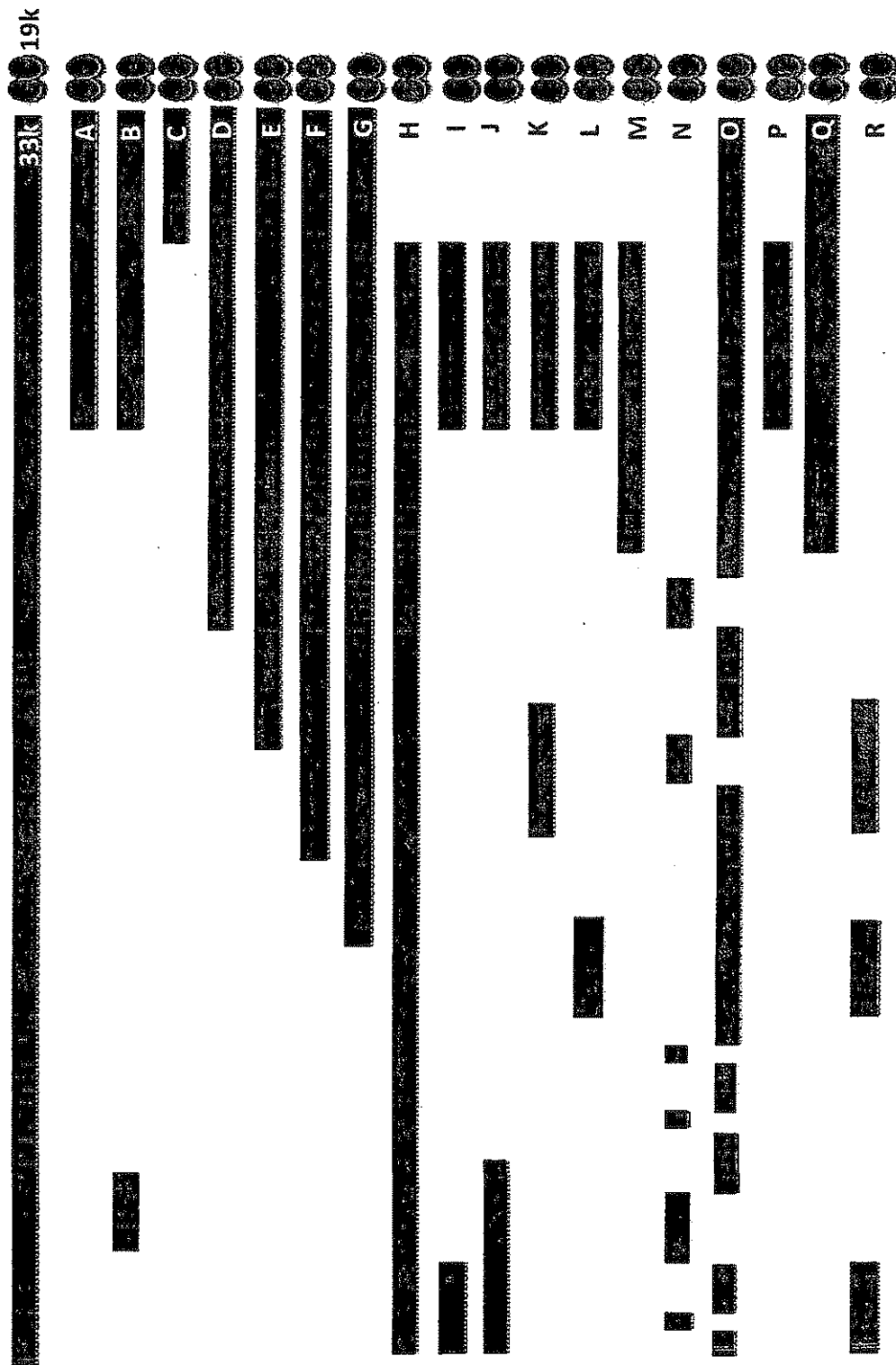


Figure 6. Diagram of all MSP-1 C-terminal constructs – ordered by Group

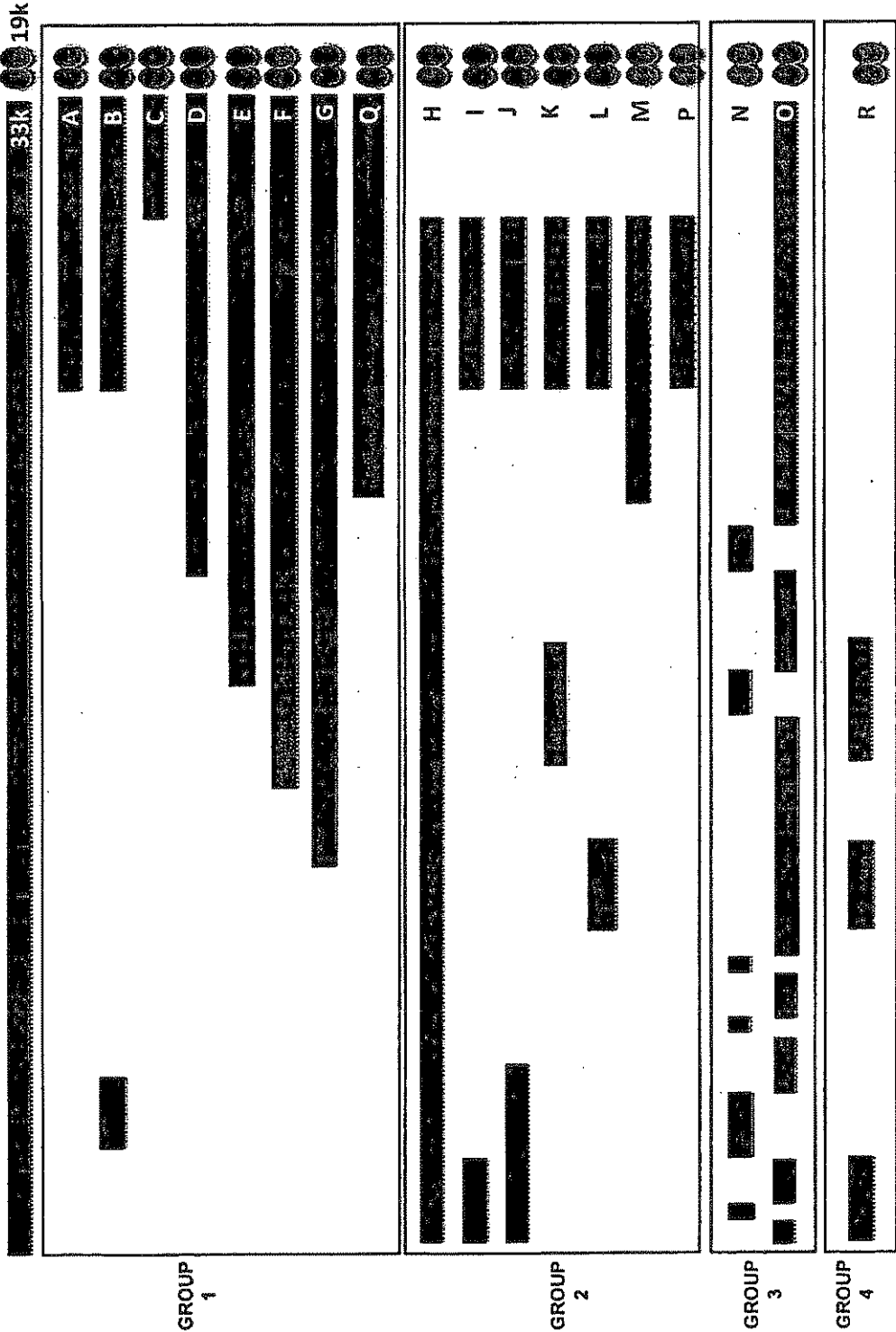


Figure 7. Mouse serum ELISA antibody titers for Group 1, 2 and 3 MSP-1 C-terminal constructs.

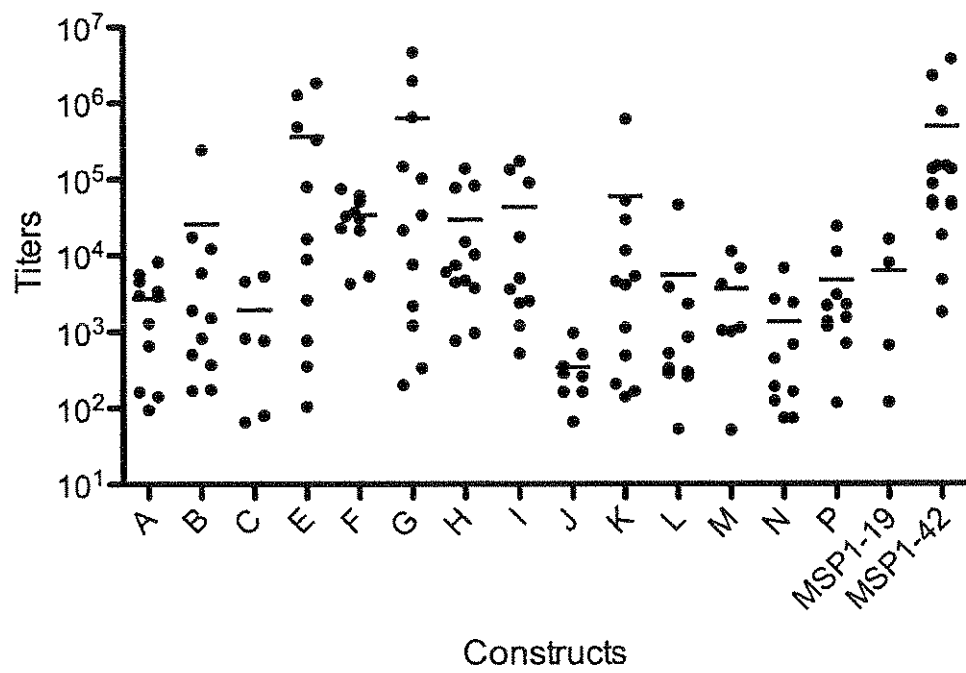


Figure 8. ELISPOT analysis of primed mouse splenocytes from Group 1, 2 and 3 MSP-1 C-terminal constructs.

